



3

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan l.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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 tctccagaca tcaacaaca atatggagaa gggtacattg aaaaagtct 850
 agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900
 tggtagagt catggaccac gctctaaca gtctcttccc taagactcat 950
 tatgccgctg gaaaagatgc caaaattttc tggatactc tgtctcacat 1000
 gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050
 ctaatcccaa ggcagtgtga ctcaagtaac cacaatgtc tcctccaggc 1100
 tatgaaattg gccgatttca agaacacatc tccttttcaa cccatttct 1150
 tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200
 agggagtccc accatcgctg gtggtatccc agggtccttg ctcaagtttt 1250
 ctttgaaaag gagggctgga atggtacatc acataggcaa gtctgacct 1300
 gtatttaggc tttgcctgct tgggtgtgat taagggaat tgaaagactt 1350
 gccattcaa aatgatcttt accgtggcct gcccatgct tatgggtccc 1400
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 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315

Pro Lys Ala Val

<210> 11

<211> 2720

<212> DNA

<213> Homo sapiens

<400> 11

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gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcctt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggacccagga ggaggccaca aaaaggcaag aagcccctgt 600
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 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900
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 atcggcta at gcctgccttc agaacacat ccaagattcc ttactcggat 1150
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 cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250
 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
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 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850
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 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
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 gtctctgtgg gccgaccaga ggggggcttc gaggtgggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctgaagc 2500
 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
 gcctgaggct ccagggttg ctctgggtgt tacaagctgg actcagggat 2600
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650
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 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

1	5	10	15
Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala	20	25	30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro	35	40	45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr	50	55	60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp	65	70	75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu	80	85	90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala	95	100	105
Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile			

	290		295		300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser		
	305	310	315		
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu		
	320	325	330		
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu		
	335	340	345		
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn		
	350	355	360		
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser		
	365	370	375		
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr		
	380	385	390		
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe		
	395	400	405		
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala		
	410	415	420		
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys		
	425	430	435		
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe		
	440	445	450		
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr		
	455	460	465		
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu		
	470	475	480		
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg		
	485	490	495		
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val		
	500	505	510		
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu		
	515	520	525		
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly		
	530	535	540		
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr		
	545	550	555		
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu		
	560	565	570		
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val		

575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn	Leu Leu Arg Pro Glu Thr	
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg Lys	
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg Phe	
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val Gln	
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe Phe	
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp Asp	
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu Ala	
680	685	690
His Pro Leu Pro Ile Trp Thr Pro Ala		
695		

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 13
 cgccagaagg gcgtgattga cgtc 24

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 14
 ccatccttct tcccagacag gccg 24

<210> 15
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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gcgcagctgc cctgggagga cggcaggctcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cgggcagtcg ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400
ctgggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accagggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtgggc ttccctggaga gcagcaacag cacggactac 550
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
tggttttcct gaggctgggc cttccacgt ggccctccccg gagctccacc 650
ctctctacca ctacaagacc tatgtcggcg gcctcctgct gctctccaag 700
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850
catgacctag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
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gtcctcaaca tcatgttgga ctgtgacaag accgccacac cctggtgcac 1050
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ggccgccaag gcaggcttgg gctggggccag gacacgtggg gtgcctggga 1250

cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcacctt actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggctga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	
				50					55					60	
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	
				65					70					75	
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	
				80					85					90	
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	
				95					100					105	
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	
				110					115					120	
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	
				125					130					135	
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu	
				140					145					150	
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp	
				155					160					165	
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala	
				170					175					180	
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His	
				185					190					195	
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His	
				200					205					210	
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly	
				215					220					225	
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu	
				230					235					240	
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe	
				245					250					255	
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg	
				260					265					270	
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly	
				275					280					285	
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu	
				290					295					300	
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp	
				305					310					315	
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser				
				320					325						

<210> 18
<211> 23
<212> DNA
<<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gcgaacgctt cgaggagtcc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcacgggcc 200
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gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18
<223> Growth factor and cytokines receptors family.

<400> 22
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1 5 10 15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23
<211> 2883
<212> DNA
<213> Homo sapiens

<400> 23
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cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccc 150
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgctcg ccccgcaggc 200
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tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaà ctgcgcgagg tcctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
 gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
 gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
 tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
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<212> PRT
<213> Homo sapiens

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<222> 1-33
<223> Signal peptide.

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<222> 13-40
<223> Transmembrane domain (type II).

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Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	
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Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	
				65					70					75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	
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Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
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				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
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				185					190					195	
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Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
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Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser
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Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp
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Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln
				365					370					375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro
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Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe
				395					400					405
Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val
				410					415					420
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr
				425					430					435
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu
				440					445					450
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu
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Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys
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Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu
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Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg
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Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile
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Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

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<210> 27

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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 <212> PRT
 <213> Homo sapiens

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 <223> Signal peptide.

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 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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 <211> 2128
 <212> DNA
 <213> Homo sapiens

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 <211> 322
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu	Ser Ala Ser Ile Ile	Tyr
110	115		120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser	His Gly Arg Ser Arg	Asp
125	130		135
His Ala Ile Ala	Ala Thr Phe Phe Ser	Cys Ile Ala Cys Val	Ala
140	145		150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg	Ala Arg Pro Gly Glu	Ile
155	160		165
Thr Gly Tyr Met	Ala Thr Val Pro Gly	Leu Leu Lys Val Leu	Glu
170	175		180
Thr Phe Val Ala	Cys Ile Ile Phe Ala	Phe Ile Ser Asp Pro	Asn
185	190		195
Leu Tyr Gln His	Gln Pro Ala Leu Glu	Trp Cys Val Ala Val	Tyr
200	205		210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile	Ala Ile Leu Leu Asn	Leu
215	220		225
Gly Glu Cys Thr	Asn Val Leu Pro Ile	Pro Phe Pro Ser Phe	Leu
230	235		240
Ser Gly Leu Ala	Leu Leu Ser Val Leu	Leu Tyr Ala Thr Ala	Leu
245	250		255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp	Glu Lys Tyr Gly Gly	Gln
260	265		270
Pro Arg Arg Ser	Arg Asp Val Ser Cys	Ser Arg Ser His Ala	Tyr
275	280		285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu	Ala Val Ala Ile Leu	Thr
290	295		300
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His Leu Val Phe	Val Lys Val		
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 <212> DNA
 <213> Homo sapiens

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg	125	130	135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys	140	145	150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp	155	160	165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala	170	175	180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly	185	190	195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu	200	205	210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser	215	220	225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu	230	235	240
Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro	245	250	255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala	260	265	270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser	275	280	285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu	290	295	300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser	305	310	315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala	320	325	330
Glu	Pro	Glu	Glu	Gln											335		

<210> 34

<211> 25

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

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 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 36
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 <210> 37
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 37
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 <210> 38
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 38
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 <210> 39
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 39
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 <210> 40
 <211> 2084

<212> DNA
<213> Homo sapiens

<400> 40

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ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105

Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val	110	115	120
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser	125	130	135
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr	140	145	150
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser	155	160	165
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val	170	175	180
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser	185	190	195
Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu	200	205	210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn	215	220	225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe	230	235	240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu	245	250	255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser	260	265	270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu	275	280	285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser	290	295	300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu	305	310	315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu	320	325	330
Arg Thr Ser Val																	

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
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aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500

tgtgtaggtg ctgaatgctg taaggagttt aggttgatg aattctacaa 1550

ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
				50					55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
				65					70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
				80					85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
				95					100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
				110					115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
				125					130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
				140					145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
				155					160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
				170					175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
				185					190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
				200					205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
				215					220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

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Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile			
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Val Glu Thr Lys Ile Cys Gln Glu			
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<210> 44
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 45
 gggaactgct atctgatgcc 20

<210> 46
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 caggatctcc tcttgacgac tgcagc 26

<210> 47
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 47
 cttctcgaac cacataagtt tgaggcag 28

<210> 48
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200
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 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
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 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

	80		85		90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala	95		100		105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln	110		115		120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys	125		130		135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe	140		145		150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala	155		160		165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170		175		180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185		190		195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200		205		210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215		220		225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230		235		240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245		250		255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260		265		270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val	275		280		

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250

ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
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<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52

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Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp	35	40	45	
Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly	50	55	60	
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr	65	70	75	
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly	80	85	90	
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala	95	100	105	
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val	110	115	120	
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val	125	130	135	
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile	140	145	150	
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro	155	160	165	
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser	170	175	180	
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln	185	190	195	
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Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln	215	220	225	
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Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly	
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Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly	
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Glu	Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn	
				350					355					360	
Met	Arg	Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser	
				365					370					375	
Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly	
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Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser	
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser	
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Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg	
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 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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<210> 54
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 54
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 Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
 35 40 45
 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
 50 55 60
 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
 65 70 75
 Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
 80 85 90
 Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
 95 100 105
 Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
 110 115 120
 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
 125 130 135
 Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
 140 145 150

Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu	155	160	165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu	170	175	180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala	185	190	195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg	200	205	210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala	215	220	225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp	230	235	240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala	245	250	255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala	260	265	270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala						275	280	

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 <211> 2401
 <212> DNA
 <213> Homo sapiens

<400> 55
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<210> 56
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 56
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 Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg Ser Arg Arg
 35 40 45
 Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
 50 55 60
 Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val
 65 70 75
 Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
 80 85 90
 Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
 95 100 105
 Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
 110 115 120
 Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
 125 130 135
 Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
 140 145 150
 Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
 155 160 165
 Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala

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Val Ser Pro Gly	Arg Met Arg Gln Phe	Asp Asp Leu Phe Arg Gly			
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Glu Thr Gly Lys	Asp Arg Glu Lys Ser	His Ser Trp Leu Ser Thr			
	200	205			210
Gly Trp Phe Thr	Met Val Ile Ala Val	Glu Leu Cys Asp His Val			
	215	220			225
His Val Tyr Gly	Met Val Pro Pro Asn	Tyr Cys Ser Gln Arg Pro			
	230	235			240
Arg Leu Gln Arg	Met Pro Tyr His Tyr	Tyr Glu Pro Lys Gly Pro			
	245	250			255
Asp Glu Cys Val	Thr Tyr Ile Gln Asn	Glu His Ser Arg Lys Gly			
	260	265			270
Asn His His Arg	Phe Ile Thr Glu Lys	Arg Val Phe Ser Ser Trp			
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Ala Gln Leu Tyr	Gly Ile Thr Phe Ser	His Pro Ser Trp Thr			
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<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57
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ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600
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aatcctctac tatgtggtga aacaccgcaa gcaggtcaca aattcctctg 1900
acgattggac catctctggc attccagcca accagaccg cctgaccctc 1950
accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacia 2000
ctgtgcggga gagggccaga cagccatggt caccttccga actggacggc 2050

ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100
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 taaggagtcc taccggttga gggtggagag ggaaaataaa gaagctgcca 3900
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 atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
 aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115
 <212> PRT
 <213> Homo sapiens

<400> 58
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 Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
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 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
 35 40 45
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
 50 55 60
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
 65 70 75
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
 80 85 90

Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
				95					100					105
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
				110					115					120
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
				125					130					135
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
				140					145					150
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
				155					160					165
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
				170					175					180
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
				185					190					195
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
				200					205					210
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
				215					220					225
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
				230					235					240
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
				245					250					255
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
				260					265					270
Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu
				275					280					285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met
				290					295					300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr
				305					310					315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser
				320					325					330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu
				335					340					345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala
				350					355					360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala
				365					370					375

Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	380	385	390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	395	400	405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	410	415	420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	425	430	435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	440	445	450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	455	460	465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	470	475	480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	485	490	495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	500	505	510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	515	520	525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	530	535	540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	545	550	555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg	560	565	570
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln	575	580	585
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp	590	595	600
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile	605	610	615
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg	620	625	630
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys	635	640	645
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665					670					675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680					685					690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695					700					705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710					715					720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725					730					735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740					745					750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755					760					765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770					775					780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785					790					795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
				800					805					810	
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
				815					820					825	
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
				830					835					840	
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
				845					850					855	
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	

Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
				950					955					960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
				965					970					975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	
				980					985					990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	
				995					1000					1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
				1010					1015					1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	
				1025					1030					1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	
				1040					1045					1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
				1055					1060					1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	
				1070					1075					1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	
				1085					1090					1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	
				1100					1105					1110	
Pro	Pro	Leu	Thr	Ile											
				1115											

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 59
 gggaacaca gcagtcattg cctgc 25

<210> 60
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 60
 gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
caccaccaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgaggagctg ggtcgatcatg atccggaccc cattgtcggc ctctgcccat 50
cgctgctcc tcccaggctc ccgcgggcca cccccgcgca acatgcagcc 100
cacggggcgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
tgctgctcct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgc 200
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250
cctcttcacc acgcccgggtg tccccagcgc cctcactacc ccaggcctca 300
ctacgccagg caccaccaaa accctggacc ttcggggctc gcgcagggcc 350
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
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cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
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agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850

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 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
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 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgctgacaca gtcgggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63
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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
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 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	
				260					265					270	
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro	
				275					280					285	
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu	
				290					295					300	
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly	
				305					310					315	
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu	
				320					325					330	
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg	
				335					340					345	

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
	350	355 360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
	365	370 375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
	380	385 390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
	395	400 405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
	410	415 420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
	425	430 435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
	440	445 450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
	455	460 465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
	470	475 480
Thr Phe Thr Gln Trp Leu Cys		
	485	

<210> 64

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
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<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
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 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
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 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
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 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
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 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
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Met Leu Ser

<210> 69

<211> 3170

<212> DNA

<213> Homo sapiens

<400> 69

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<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
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35 40 45
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75
Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90
His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105
Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130					135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
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Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

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<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72

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				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
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Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
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Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
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Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
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Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
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Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
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Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
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Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
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Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
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Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
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Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

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Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn					
	305		310		315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr					
	320		325		330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg					
	335		340		345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp					
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Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 73
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<210> 74
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 <212> DNA
 <213> Artificial Sequence

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<400> 74
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<210> 75
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 75
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<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 76

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caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu	35	40	45	
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro	50	55	60	
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val	65	70	75	
Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90	
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105	
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120	
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135	

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150

cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250
 cactgccaag gactactgga tgttcaaact ccgcaactcc tccagcccag 300
 ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350
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 ctctctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450
 tgacgggtcat cctggccatc ttcatgggtga taactgcact ggtgaaggtg 500
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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys	395	400	405
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser	410	415	420

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430					435
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

<210> 80
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 80
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<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844
 <212> DNA
 <213> Homo sapiens

<400> 83
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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84
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20 25 30
Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
35 40 45
Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
50 55 60
Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
65 70 75
Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
80 85 90
Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
95 100 105
Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
110 115 120
His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
125 130 135
Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
140 145 150
Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
155 160 165
Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
170 175 180
Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
185 190 195

Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr
				200					205					210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala
				215					220					225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr
				230					235					240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp
				245					250					255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro
				260					265					270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala
				275					280					285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln
				290					295					300
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala
				305					310					315
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile
				320					325					330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg
				335					340					345
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg
				350					355					360
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn
				365					370					375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu
				380					385					390
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala
				395					400					405
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu
				410					415					420
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp
				425					430					435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser
				440					445					450
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu
				455					460					465
Lys	Asp	Asp	Trp	Thr	Val	Pro	Tyr	Gly	Arg	Ile	Tyr	Phe	Ala	Gly
				470					475					480

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
				545					550					555
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
				560					565					

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 ggagcacgga aggggggtttc ccagaagaac aatgacctaa caagttgctg 450
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
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Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys	65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg	80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val	95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn	110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu	125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu	140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys	155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His	170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala	185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr	200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu	215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile	230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu	245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro	260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu	275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe	290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys	305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr			

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Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
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Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
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Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
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Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
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Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
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Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
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Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
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Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
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Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
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Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
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Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
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Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
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Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
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Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		

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Asn Ile Tyr Asn	Arg Ser Gln Pro Val	Leu Gln Ile Phe Val	His		
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Gly Glu Ser Leu	Arg Ser Ser Leu Val	Gly Val Val Val Pro	Asp		
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Thr Asp Val Leu	Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys	Gly		
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Ser Phe Glu Glu	Leu Cys Gln Asn Gln	Val Val Arg Glu Ala	Ile		
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Leu Glu Asp Leu	Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys	Thr		
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Phe Glu Gln Val	Lys Ala Ile Phe Leu	His Pro Glu Pro Phe	Ser		
	695		700		705
Ile Glu Asn Gly	Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg	Gly		
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Glu Leu Ser Lys	Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr	Glu		
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His Ile Gln Asp

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

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<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

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Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
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Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
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Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
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Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn
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Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser
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Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp
				200					205					210
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His
				215					220					225
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				230					235					240
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His
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Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro
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Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met
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Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	395	400	405
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Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly	440	445	450
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Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg	470	475	480
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Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly	500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val	515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala	530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu	545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr	560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp	575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp	590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe	605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro	620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu	635	640	645
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35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
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Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
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Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
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Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210

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Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val
				230					235					240
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
				245					250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
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Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
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Leu	Ser	Val	Gly	His	Gln	His								
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 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

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<220>
 <223> Synthetic oligonucleotide probe

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<210> 99
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<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgccccctcg tgctggccgc cctggtggcc tgcattcatcg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tggagctgga aggcagggtc cgcaggggcg ctgcagagag aggcgccgtg 300
gagctgaaga agaacgagtt ccaggggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgct gcaagaccag ttaaagacct tgcagaggaa 500
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ggaatcatat actctgaatt gaactggaat cacatatattt acaacagggc 1350

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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230.	235	240
Glu Val Val Leu Asp Ser Lys Arg Gln	Val Glu Lys Glu Glu Thr	
245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu	Pro Gln Arg Asp Arg Leu	
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val	Val Glu Asp Arg Pro Val	
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly	Glu Leu Gly Gln Thr Pro	
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu Met	
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys	Arg Asp Thr Ile Asn Leu	
380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His	Thr Leu	
395	400	

<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
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Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
				215					220					225	
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
				230					235					240	
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	
				245					250					255	
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
				260					265					270	
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp	
				275					280					285	
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
				290					295					300	
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
				305					310					315	
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
				320					325					330	
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
				335					340					345	
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	
				350					355					360	
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	
				365					370					375	
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
				380					385					390	
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
				395					400					405	
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
				410					415					420	
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
				425					430					435	
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
				440					445					450	

Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	
				455					460					465	
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	
				470					475					480	
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	
				485					490					495	
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
				500					505					510	
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
				530					535					540	
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
				545					550					555	
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
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Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
				575					580					585	
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
				590					595					600	
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
				605					610					615	
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
				620					625					630	
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
				635					640					645	
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
				650					655					660	
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
				665					670					675	
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
				680					685					690	
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
				695					700					705	
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
				710					715					720	
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
				725					730					735	

Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu	
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Ala	Ala	Ser	Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val	
				755					760					765	
Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu	
				770					775					780	
Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr	
				785					790					795	
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly	
				800					805					810	
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala	
				815					820					825	
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu	
				830					835					840	
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile	
				845					850					855	
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu	
				860					865					870	
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe	
				875					880					885	
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr	
				890					895					900	
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile	
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His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser	
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Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala	
				935					940					945	
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp	
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Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu	
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Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu	
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Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
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Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
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Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
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Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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<210> 103
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 atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
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 gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
 aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750
 atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
 ccttaatgat cctcagcca gcgggaacct gagggcccct caggaggaag 850
 aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900

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cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atggtgggcc 1650
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aatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
<211> 442
<212> PRT
<213> Homo sapiens

<400> 104
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20 25 30
Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
35 40 45
Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
50 55 60
Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
65 70 75
Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
80 85 90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser
				380					385					390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly
				395					400					405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro
				410					415					420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly
				425					430					435
Leu	Tyr	Val	Gln	Met	Glu	Asn								
				440										

<210> 105
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 105
 cgctgctgct gttgctcctg g 21

<210> 106
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 106
 cagtgtgccca ggactttg 18

<210> 107
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 107
 agtcgcaggc agcgttgg 18

<210> 108
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 108

ctcctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgtgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

agggcctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300

acagagacct ccgcactggc ctggtggtgc tgggcgccca cgtcctgagt 350

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ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500

gggagaaggg ccaggcccc cacagcgggg acacggtgcc ggggtggctgg 550

ctggggcttc gtgtctgact ttgaggagct gccgctgga ctgatggagg 600

ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650

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ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
 gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
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 aaaaaaaaaa gaaa 1114

<210> 111
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 111

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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg

	200	205	210
Arg Gly Phe Cys	Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys	Arg
	215	220	225
Asn Arg Ala His	Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys	Gly
	230	235	240
Asp Pro Lys Thr	Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe	Val
	245	250	255
Ala Trp Ile Trp	Asp Val Val Arg Arg	Ser Ser Pro Gln Pro	Gly
	260	265	270
Pro Leu Pro Gly	Thr Thr Arg Pro Pro	Gly Glu Ala Ala	
	275	280	

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

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cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200
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caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	
				230					235					240	
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
				245					250					255	
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
				260					265					270	
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
				275					280					285	
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
				290					295					300	
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
				305					310					315	
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	
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Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
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 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
 agcgccggtt gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200
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 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
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 tccagccttt gaggacctg agggagcagc aagggccctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
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 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr
				470					475					480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp
				485					490					495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His
				500					505					510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys
				515					520					525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser
				530					535					540

Ser Pro Glu Asp

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 119
 cgggacagga gacccagaaa ggg 23

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122

gagatagggga gtctggggttt aagttcctgc tccatctcag gagccccctgc 50
tcccacccct aggaagccac cagactccac ggtgtggggc caatcagggtg 100
gaatcggccc tggcagggtg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taacccgcgc ggggagcgcc caggatgccg 200
cgcggggact cggagcagggt gcgctactgc gcgcgcttct cctacctctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
gggegctgct atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgtctgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
cgactgcagt gcccctggac ccctggcctg tgggggtgcc tacacctgct 750
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
atcgacaagg agcgtttcag tgtgcaggat gtcacttacg tgcggggctg 850
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
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 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650
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 catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe
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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly

	170		175		180									
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly
				230					235					240
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

atcatctatt ccaccgtggt ctggc 25

<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatctatg cagaggttga ggggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta 350
acatcctcca gctgcaggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcgc tggctcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttctt 600
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cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000
cttcttgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050
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aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200
caccctgggc atcgaagcca gctcgggaagc tcagttttac accaaagggtg 1250

accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
 cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
 gatctgggggt cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450
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 gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20						25					30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35						40					45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
			50						55					60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65						70					75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80						85					90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95						100					105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110						115					120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125						130					135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140						145					150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155						160					165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu

				170						175					180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	
				185					190					195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	
				200					205					210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	
				215					220					225	
Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	
				230					235					240	
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	
				245					250					255	
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	
				260					265					270	
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	
				275					280					285	
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	
				290					295					300	
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	
				305					310					315	
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	
				320					325					330	
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	
				335					340					345	
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	
				350					355					360	
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	
				365					370					375	
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	
				380					385					390	
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	
				395					400					405	
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	
				410					415					420	
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	
				425					430					435	
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	
				440					445					450	
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	

455	460	465
Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser		
470	475	480

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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 aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
 agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
 ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
 aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450
 ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
 tagacccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
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 aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
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 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
 tttgtagctg aaacacacat tggtcttctg tttaatggtg gagttacctt 850
 aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
 agcgaaagat aatgtgtgtg gctggatttg gacttggtgt attattcttc 950
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gtatattttg tattacctct ttttttcaag tgatttaaag agttaatcat 1150
 ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200
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 aactactact ttgttttagt tagaacaag ctcaaaacta ctttagtta 1350
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 cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450
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 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
 tgaggcacga gaatcacttg aactcaggag atggaggttt cagtgagccg 2150
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln

	20		25		30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met	35		40		45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys	50		55		60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile	65		70		75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys	80		85		90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg	95		100		105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp	110		115		120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser	125		130		135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg	140		145		150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln	155		160		165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val	170		175		180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu	185		190		195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met	200		205		210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys	215		220		225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg	230		235		240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn	245		250		255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His	260		265		270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu	275		280		285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys	290		295		300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser					

	305		310		315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr					
	320		325		330
Ser Phe Leu Met Ser					
	335				

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
 aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50
 ctgctagggga gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100
 tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcattggaga ggcattggcta ccgaacacag aaatttggga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600
 taatcttatt cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
 tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900
 aaactgcact ggaagattta caaaaaaga aattaagaat attagagcat 950
 tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100

gcatgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350
 tgtgaatgcc tccacctaca tgcttcgaac taacctctgg aaatatatag 1400
 cctattcgga tgggtgcatca atattgcctc aactctttga tctttcctcg 1450
 gatccagatg aattaacaaa tggtgctgta aaatttccag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550
 cttctgtcca ccagtataat aaagagcagt ttatcaagt gaaacaaagt 1600
 ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
 ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800
 atgaaacagt ttaataatt accaagtttt ggccgggcac agtggctcac 1850
 acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggctc 1900
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 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
 tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggg gaaaaaaaaa aaaaaaaaaa 2400
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 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala	
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25						30
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40						45
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55						60
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70						75
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85						90
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100						105
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115						120
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130						135
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145						150
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160						165
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175						180
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190						195
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205						210
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220						225
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235						240
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250						255

Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	260	265	270
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	275	280	285
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	290	295	300
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	305	310	315
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	320	325	330
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	335	340	345
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	350	355	360
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	365	370	375
Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Glu	Thr	Phe	Lys	380	385	390
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser	395	400	405
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg	410	415	420
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile	425	430	435
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr	440	445	450
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln	455	460	465
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val	470	475	480
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile	485	490	495
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln	500	505	510
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln	515	520	525
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val					530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
gagagaagtc agcctggcag agagactctg aaatgaggga ttagaggtgt 50
tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100
gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctccctccctg 400
gcctgcatta tctctgtggg gggcatgaga tgcacagtct tctgccagga 450
atccccagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
tgagagaggc ctttacttgg gcattatttc ttccctgttc tccctgatag 650
ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850
gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccctggaacc tccatccac tcttggtatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
 50 55 60
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
 65 70 75
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
 80 85 90
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
 95 100 105
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
 110 115 120
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
 125 130 135
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
 140 145 150
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
 155 160 165
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
 170 175 180
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
 185 190 195
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
 200 205 210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
215 220 225

Leu Thr Gly Tyr Val
230

<210> 135
<211> 610
<212> DNA
<213> Homo sapiens

<400> 135
gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50
cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100
aagtcacgc tcccgtggc tcagaacat ggctgtgcca gccggcacc 150
aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
cgccatcgtg tccctgagcg agaccgcca atgtgggtccc cctgcacct 250
tctggccctg ctttgagctc tgctgtcttg attccttttg cctcaciaac 300
gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350
atctcccatc tccagtaa at gtgaaagcag aagacgtttt cctgagaag 400
acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
acctgtaaaa 610

<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
1 5 10 15
Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30
Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45
Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60
Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

				65						70					75
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe	
				80					85					90	
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser	
				95					100					105	
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro		
				110					115						

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250
 ctgctttgag cagtgctgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctacgcccgg acctcgatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
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 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaagge tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataaatgaaa a 771

<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	
			20					25						30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
			35					40						45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
			50					55						60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
			65					70						75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
			80					85						90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
			95					100						105	
Cys	Arg	Ser	Val	Ser											
			110												

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139
 gggggcggggt gcctggagca cggcgctggg gccgcccgc gcgctcactc 50
 gctcgactc agtcgcggga ggcttccccg cgccggccgc gtcccgcccg 100
 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250
 cgccgtattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatgggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750

ggaatcctct gcctccccct catcctgctc ctgggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900
 atacccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950
 gccttctgag tctgggcggc atctgctttc ggagcccagc acccccctgt 1000
 ctccctccagg ccccgagagac gtctttcttc catccctgga cctgtccct 1050
 gactctccaa actttgaggt catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggtt ggctctgtga 1150
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250
 atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450
 tggggcacc cccagggcac cagacacagg gcacgggtga gagacttctc 1500
 ccccgtaggc gccttggtc cccggttttg cccgaggctg ctcttctgtc 1550
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgcca 1600
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650
 gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800
 gttgccccac cactggaga tgggtgctgag ggaggtgggt ggggccttct 1850
 gggaaggatga gtggagaggg gcacctgcc cccgccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly
1				5					10					15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val
				20					25					30
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro
				35					40					45
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val
				50					55					60
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser
				65					70					75
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg
				80					85					90
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln
				95					100					105
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu
				110					115					120
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn
				125					130					135
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu
				140					145					150
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu
				155					160					165
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val
				170					175					180
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala
				185					190					195
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu
				200					205					210
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg
				215					220					225
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile
				230					235					240
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro
				245					250					255
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln
				260					265					270
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
 cccacgcgtc cgcgcctctc ccttctgctg gaccttcctt cgtctctcca 50
 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100
 cttagacctc ccttctgcc ctcctttcct gccaccgct gcttctggc 150
 ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200
 tctgtggccc ctgtgectcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccgg accagcggcc tgaccctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350
 actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcaccac tacttgagc cacaaggcct 450
 gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
 accgectcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
 cagcaatgct gtcccaagtg tgtggaacct cacactcct ctggactccg 600
 ggccccacca aagtctgcc agcacaacgg gaccatgtac caacacggag 650
 agatcttcag tgcccatgag ctgttcccct cccgctgcc caaccagtgt 700
 gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
 cccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
 cagtcgctcc atgggggtgag acatcctcag gatccatgtt ccagtgatgc 900
 tgggagaaag agaggcccgg gcacccacgc cccactggc ctcagcgccc 950
 ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
 cggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100

tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
 tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
 agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
 ctcgtccaca catcgggtatc cccaagccca gacaacctgc gtcgctttgc 1350
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
 ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
 gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
 gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
 <211> 451
 <212> PRT
 <213> Homo sapiens

<400> 142
 Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1 5 10 15
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
 20 25 30
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	290	295	300
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	305	310	315
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	320	325	330
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	335	340	345
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	350	355	360
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	365	370	375
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	380	385	390
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	395	400	405

Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro
				410					415					420
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala
				425					430					435
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys
				440					445					450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
 cttagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50
 cggggagctc ccgtgggagc tccgctggct gtgcaggcgg ccatggattc 100
 cttgcggaaa atgctgatct cagtcgcaat gctgggagca ggggctggcg 150
 tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggagccg 400
 gaccttggct tgggagcagg aatccgaggc agcctttctc cttcgtgggc 450
 ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 tttaaggtcc gcaaggcggg ccaggggcga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90

Arg Ser Pro

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50

ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100

caggctgcca tggggcccag caccctctc ctcactttgt tccttttgtc 150

atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200

aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250

agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300

actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350

acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaagggtgac 450

tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500

tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550

ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600

gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650

ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700

gcttcccag tccgggtgcc ctccccctgg gtaggcacag ggcagctggg 750

atatggtggc tttctttatt ttgctcggag gcctcctgga agacctgggtg 800

gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850

aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900

cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
 tctatgtcgt ctataacacc cgtcctgcca gtcggggccc catccagtgc 1150
 tcctttgatg ccagcggcac cctgaccctt gaacgggcag cactccctta 1200
 ttttccccgc agatatgggtg cccatgccag cctccgctat aacccccgag 1250
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
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 ttctcattc ttcaaagtgt gccagttgt ggctcaaac ctctatat 1450
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 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
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 cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
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 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5				10					15	

Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
			20					25					30	

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35				40						45	

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala
				260					265					270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile

	335		340		345
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala					
	350		355		360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu					
	365		370		375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly					
	380		385		390
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu					
	395		400		405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttgggtggg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcgc atctctctga ggctggaaaa cattactgtg 500
 ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggg tccccgggc cacagcgaag tggaaaggc cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgttttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850

aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttata agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
 aatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctc ctcccagatc caaagtcccg 1750
 cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac 1800
 atgggagtea ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950
 tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
 acagagtgta tcctaattgg ttgttcatta tattacactt tcagtaaaaa 2050
 aa 2052

<210> 148
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val	Gln Ala
	20	25	30
Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser	Pro Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly	Gln Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln	Pro Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val	Lys Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn	Ile Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser	Gln Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala	Leu Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg	Asp Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro	Thr Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp	Ser Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile	Ser Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met	Arg His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile	Gly Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys	Val Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly	Leu Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu	Leu Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala	Arg Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His	Pro Lys

290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 150

ggaactgacc cagtgtgac acc 23

<210> 151

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 151

gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152

<211> 2294

<212> DNA

<213> Homo sapiens

<400> 152

gcgatggtgc gcccggtggc ggtggcgccg gcggttgccg aggccttcctt 50

ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100

aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctggggc 150

gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200

gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250

cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300

gggcgaaggc tcccacggcc caggccccga ggaccgggccc ccgcgcgcc 350

accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacctctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450

cgtcggccc ctcgccgacc acccctccgg cggcggaacg cacttcgacc 500

acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550

tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600

ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650

ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700

tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750

agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800

gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaataa 950
aaaaggctgc tactctcaag gaccatactg gtttaaaca aggaggatga 1000
gggtcataga ttacaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaattttt ctctgggata atttctgtaa 1150
atctcatggg aaaaaattat tgaagaataa atctgctttc tggaagggt 1200
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300
taatcaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggg acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
tggttataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaagggtg ttgtgaagat 1750
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ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850
tggttttaaga acttttagct ccttgacaaa gaagtgtttt atacttttagc 1900
actaaatatt ttaaatagct tataaatgat attatactgt tatggaatat 1950
tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
ctcacgcctg taatcctagc actttgggag gccaaggcgg gtggatcact 2050
tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100
ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgtag 2150
tcccagctac tcgggagggt gaggcaggag aatcggttga acccgaggag 2200

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15

Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cagtcacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 156
aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggcttt ggtctcgggtg cccagggccc aggccgtgtg gttgggaaga 100
ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtaggcctc 150
ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200
tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
tgctggccac caacttcaga gactatgcc a tcatcttcac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
gggtcctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650
gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1 5 10 15
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
20 25 30
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90
Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105
Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120
Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135
Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150
Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665
<212> DNA
<213> Homo sapiens

<400> 159
aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacct 200
tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaattctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacacccct atgatctct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950
gggtctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100
tggagccaca gccctgggtc tctgtcctt ctgcgtcatc ttcgtttag 1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatag aggatgcaaa cgctgtcagg gggtcagcct ctacggggcc 1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgcccg.ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350
agcttccaga tgggtgaagcc ttgggactcg cggggacagg aggccactga 1400
caccgagtag tcggagatca agatccacag atgagaaaact gcagagactc 1450
accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	
1				5					10					15	
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	
				20					25					30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	
				35					40					45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	
				50					55					60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	
				65					70					75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	
				80					85					90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	
				95					100					105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	
				110					115					120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	
				125					130					135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	
				140					145					150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	
				155					160					165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	
				170					175					180	

Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser	185	190	195
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser	200	205	210
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn	215	220	225
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr	230	235	240
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly	245	250	255
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu	260	265	270
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu	275	280	285
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser	290	295	300
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala	305	310	315
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln	320	325	330
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val	335	340	345
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe	350	355	360
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys	365	370	375
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu	380	385	390
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr	395	400	405
Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala	410	415	420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser	425	430	435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu	440	445	450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg			455	460	

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgccagtg gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatgggtgg 150
 tcgataagga ctttccggag gacaggaggg ccaggaaggt gtccccagtg 200
 aaggtgacag ccctggggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggaggggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550
 acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttccct 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
 20 25 30
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
 35 40 45
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
 50 55 60
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
 65 70 75

Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	
				80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	
				95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	
				110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	
				125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	
				140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	
				155					160					165	
Cys	Val	Pro	Glu	His											
				170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 165
 gtcctccgga aagtccttat c 21

<210> 166
 <211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggacctg gtacgtgaag gccatgggtg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gttccgcaga tgcagagggt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccgagacag ccactgagtc cttccccac cccggcttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctgggtgaag 450
atggcatcgc cagtctccat cacctggggt gtgcgacccc tcaccctctc 500

ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
 cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccaggggtga ctccgggggc cctctgggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctgggtgt 800
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcacctc catttccact 900
 tgggtgtttgg ttctgtttca ctctgttaat aagaaaccct aagccaagac 950
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
 tgtatcccca gcccacaaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu
1				5					10					15
Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro
				20					25					30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu
				35					40					45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala
				50					55					60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His
				65					70					75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr
				80					85					90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys
				95					100					105

Asp His Arg Asn Asp Ile Met Leu Val	Lys Met Ala Ser Pro Val
110	115 120
Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys	
125	130 135
Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr	
140	145 150
Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn	
155	160 165
Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly	
170	175 180
Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly	
185	190 195
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn	
200	205 210
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala	
215	220 225
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val	
230	235 240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn	
245	250

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcggga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
cgtgtagaca ccaggctttc gggtg 25

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctggtc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150
agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
tgtgaccaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
atttctactt ttttttttta gctatttact gtactttatg tataaaaca 750
agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
ttttgatctc cccaatacat tgatttttgt ataataaatg tgaggctgtt 850
ttgcaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 182
 gacatggaca atgacagg 18

 <210> 183
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 183
 cctttcagga tgtaggag 18

 <210> 184
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 184
 gatgtctgcc accccaag 18

 <210> 185
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 185
 gcacacctgat atgacttgct acgtggc 27

 <210> 186
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 186
 tacaagaggg aagaggagtt gcac 24

 <210> 187
 <211> 52
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaagtct tctgtgtca ataactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggtgagggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
1 5 10 15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
agggaccatt gcttcttcca ggcc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
 gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
 gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
 cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700
 atgcctgcca ggggtgattct gggggccccc tgggtgtgtgg gggagtcctt 750
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800
 ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatacttc 950
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagacca cgagcgggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	
				125					130					135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	
				140					145					150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	
				155					160					165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	
				170					175					180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	
				185					190					195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	
				200					205					210	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	
				215					220					225	
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	
				230					235					240	
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn								
				245											

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagaggtg acaggagggg 400
 tcagtgcac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600

ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgttttgt cattgagggt ttgttttgtt tttcatcaat gtctttgtaa 700
 agcacaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
 ttgggtcccc tccctctctt ctccctcctt tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850
 cttccagcct gtgttcccct cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
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 acccaggaca cagccactcg gggccccgct gcccagctg atccccactc 1100
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 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgct 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197
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 cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
 ggggtcggcg ccgccgtgcg cggccgcctg gcgctggcct tggcgctggc 150
 gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
 gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttctt 250
 cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
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 tgcattctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
 gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
 ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
 tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550
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 agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
 acaacaacat cagtcgcctc ctgggtcacca gcttcaacca catgccgaag 700
 atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750
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 cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggtatgtg 850
 cagaagaagg agtacgtgtg cccagcccc cactcggagc ccccatcctg 900

caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950
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 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050
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 agaatcagat atcggatatt gctccagatg ccttccaggg cctgaaatca 1150
 ctcacatcgc tggctcctgta tgggaacaag atcaccgaga ttgccaaggg 1200
 actgtttgat gggctgggtg ccctacagct gctcctcctc aatgccaaca 1250
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 tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450
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 attaccgcag caggttcagc agcgagtgtc tcatggacct cgtgtgcccc 1600
 gagaagtgtc gctgtgaggg cacgattgtg gactgctcca accagaagct 1650
 ggtccgcac ccaagccacc tccctgaata tgtcaccgac ctgcgactga 1700
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 cccaacctgc ggaaaataaa tctgagtaac aataagatca aggaggtgcg 1800
 agagggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850
 ggaaccagct ggagaccgtg cacggggcgcg tgttccgtgg cctcagtggc 1900
 ctcaaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950
 cacctttgcc ggctgagtt cggtgagact gctgtccctc tatgacaatc 2000
 ggatcaccac catcaccctt ggggccttca ccacgcttgt ctccctgtcc 2050
 accataaacc tctgtccaa ccccttcaac tgcaactgcc acctggcctg 2100
 gctcggcàag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150
 gccagaagcc atttttcctc aaggagattc ccatccagga tgtggccatc 2200
 caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250
 gcgctgcccc gagcagtgc cctgtatgga gacagtgggt cgatgcagca 2300
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ctgtacctgg aaggaaacca cctaacagcc gtgcccagag agctgtccgc 2400
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<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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				20					25					30

Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
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	35	40	45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro	50	55	60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg	65	70	75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu	80	85	90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe	95	100	105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys	110	115	120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu	125	130	135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg	140	145	150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp	155	160	165
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr			

320					325					330				
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp
				335					340					345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu
				350					355					360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe
				365					370					375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys
				380					385					390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu
				395					400					405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys
				410					415					420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala
				425					430					435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp
				440					445					450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser
				455					460					465
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn

605										610				615			
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser			
				620					625					630			
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr			
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Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu			
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Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly			
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Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys			
				680					685					690			
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala			
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Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln			
				710					715					720			
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val			
				725					730					735			
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met			
				740					745					750			
Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr			
				755					760					765			
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile			
				770					775					780			
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe			
				785					790					795			
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg			
				800					805					810			
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu			
				815					820					825			
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu			
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Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly			
				845					850					855			
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu			
				860					865					870			
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser			
				875					880					885			
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr			

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Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr
920					925					930				
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr
935					940					945				
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile
950					955					960				
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser
965					970					975				
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly
980					985					990				
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys
995					1000					1005				
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys
1010					1015					1020				
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile
1025					1030					1035				
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys
1040					1045					1050				
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly
1055					1060					1065				
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala
1070					1075					1080				
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly
1085					1090					1095				
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu
1100					1105					1110				
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln
1115					1120					1125				
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu
1130					1135					1140				
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu
1145					1150					1155				
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu
1160					1165					1170				
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
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Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
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Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
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Glu Cys Gly Cys Leu Ala Cys Ser		
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 199
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<210> 200
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 200
 ttgttggcat tgaggaggag cagc 24

<210> 201
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
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 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

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 <212> DNA
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gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
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 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
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<211> 148

<212> PRT

<213> Homo sapiens

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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
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Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
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<212> DNA

<213> Homo sapiens

<400> 209

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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200

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cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800

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aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100

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 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
 ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcaactgtcat ctgtaggga atttttgttt gtcctgtctt tgcctggatc 1550
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<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly
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Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val
				20					25					30
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
				35					40					45
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
				50					55					60
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
				65					70					75
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
				80					85					90
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
				95					100					105
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
				110					115					120
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
				125					130					135
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
				140					145					150
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp

	155	160	165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu	Arg
	170	175	180
Val Leu Glu Asn	Val Glu His Tyr Gln	Glu Leu Lys Lys Met	Val
	185	190	195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser	Phe
	200	205	210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys	Val
	215	220	225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu	Glu
	230	235	240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly	Gly
	245	250	255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys	Glu
	260	265	270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile	Arg
	275	280	285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala	Arg
	290	295	300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu	Tyr
	305	310	315
Arg Tyr Val Thr	Lys Leu Leu Val		
	320		

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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tctacctcta tccggcttcc agacaagctg caggaattcc aggattact 150

ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200

tttgcacgag ttcttggtta atttgcacga gagatatggg cctgtggtct 250

ccttctgggtt tggcaggcgc ctctgtggtta gtttgggcac tggtgatgta 300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350

gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
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 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
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 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
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<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	
				20					25					30	
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	
				35					40					45	
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	
				50					55					60	
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	
				65					70					75	
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	
				80					85					90	
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	
				95					100					105	
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	
				110					115					120	
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	
				125					130					135	
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	
				140					145					150	
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser	
				155					160					165	
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val	
				170					175					180	
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln	
				185					190					195	
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu	
				200					205					210	
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu	
				215					220					225	
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys	
				230					235					240	
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser	
				245					250					255	
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser	
				260					265					270	
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
				275					280					285	
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	
				290					295					300	

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305					310					315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320					325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335					340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350					355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365					370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380					385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395					400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410					415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425					430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440					445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455					460						

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tcagggcttg tgccctctcg cttcctgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
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 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggtt 600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
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tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
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Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggcttact ggcctgcggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	1	5	10	15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	20	25	30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	35	40	45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	50	55	60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	65	70	75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	80	85	90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	95	100	105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	110	115	120	

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200
gcggggccac atctcaccta agtcccgcce catggccaat tccactctcc 250
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gtccagaagg tgtgcccaga ttacaactac catagtata cccctacta 800
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ggacaggcct gcccatgcag gagaccatct ggacaccggg caggggaagg 900
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 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
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 aataaagctt gccccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218
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 Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
 20 25 30
 Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	
				50					55					60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	
				65					70					75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	
				80					85					90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	
				95					100					105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	
				110					115					120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	
				125					130					135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	
				140					145					150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	
				155					160					165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	
				170					175					180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	
				185					190					195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	
				200					205					210	
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	
				215					220					225	
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	
				230					235					240	
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				
				245					250						

<210> 219
 <211> 2065
 <212> DNA
 <213> Homo sapiens

<400> 219
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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gcgcccgcgc cgccgctcgt cctgcagcgc tgtcgacctc gccgctagca 250
 tcttcccagag caccgggagc ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgccagcc ggcctgcggct gcccacacgg ctcacatgg gctccgggcg 350
 ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
 aagtgtctgg tgggtgtgca ctggaacccg gccacggact ccaagggctc 500
 ctcttctctc ccgctgggga tatcgggtccg ggcgggccaac tccaaggtcg 550
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 aagacgcgca tcatttactt cgatcagatc ctgggtgaatg tgggtaattt 650
 tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
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 gaattttatt tgttttagttt taaaagactg gcaaccagggt ctaaggatta 1300
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<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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				20				25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55						60
Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala
				65				70						75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr
				80				85						90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe
				95				100						105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr
				110				115						120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile
				125				130						135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe
				140				145						150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val
				155				160						165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
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Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
185 190 195

Phe Leu Val Phe Pro Leu
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<220>
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<400> 222
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<210> 223
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 224
<211> 902
<212> DNA
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
 tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
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<210> 225

<211> 257

<212> PRT

<213> Homo sapiens

<400> 225

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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20					25					30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40					45
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
				50					55					60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65					70					75
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95					100					105

Pro Gly Glu Thr	Ala Pro Ser Met Arg	Leu Leu Ala Tyr Val	Ser
110	115		120
Gly Leu Gly Phe	Gly Ile Met Ser Gly	Val Phe Ser Phe Val	Asn
125	130		135
Thr Leu Ser Asp	Ser Leu Gly Pro Gly	Thr Val Gly Ile His	Gly
140	145		150
Asp Ser Pro Gln	Phe Phe Leu Tyr Ser	Ala Phe Met Thr Leu	Val
155	160		165
Ile Ile Leu Leu	His Val Phe Trp Gly	Ile Val Phe Phe Asp	Gly
170	175		180
Cys Glu Lys Lys	Lys Trp Gly Ile Leu	Leu Ile Val Leu Leu	Thr
185	190		195
His Leu Leu Val	Ser Ala Gln Thr Phe	Ile Ser Ser Tyr Tyr	Gly
200	205		210
Ile Asn Leu Ala	Ser Ala Phe Ile Ile	Leu Val Leu Met Gly	Thr
215	220		225
Trp Ala Phe Leu	Ala Ala Gly Gly Ser	Cys Arg Ser Leu Lys	Leu
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Cys Leu Leu Cys	Gln Asp Lys Asn Phe	Leu Leu Tyr Asn Gln	Arg
245	250		255

Ser Arg

<210> 226

<211> 3939

<212> DNA

<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200

tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250

gtctgtgaac gtcctgaaca agcagaaggg ggcgccgttg ctgtttgtgg 300

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gggatgtttc agcgcaagta cctctaccaa aaagtggaac gaaccctgtg 400

tcagccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450

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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30
Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser
				35					40					45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn
				50					55					60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
				65					70					75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
				80					85					90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
				95					100					105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
				110					115					120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser

				125					130					135	
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	
				140					145					150	
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	
				155					160					165	
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	
				170					175					180	
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	
				185					190					195	
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	
				200					205					210	
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	
				215					220					225	
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	
				230					235					240	
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	
				245					250					255	
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	
				260					265					270	
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	
				275					280					285	
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	
				290					295					300	
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	
				305					310					315	
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala	
				320					325					330	
Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro	Arg	Val	Leu	Ala	
				335					340					345	
Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly	
				350					355					360	
Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser	
				365					370					375	
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg	Ser	Phe	
				380					385					390	
Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val	
				395					400					405	
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	

				410					415					420
Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala
				425					430					435
Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe
				440					445					450
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val
				455					460					465
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn
				470					475					480
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly
				485					490					495
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile
				500					505					510
Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile
				515					520					525
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu
				530					535					540
Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr
				545					550					555
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys
				560					565					570
Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met
				575					580					585
Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro
				590					595					600
Asp	Ile	Asn	Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile
				605					610					615
Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn
				620					625					630
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr
				635					640					645
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu
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Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp
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Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val
				680					685					690
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Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile
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Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu
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Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe
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Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser
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His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser
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Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln
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 <213> Homo sapiens

<400> 228
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
				35					40					45
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala

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Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val			
				95					100					105			
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn			
				110					115					120			
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu			
				125					130					135			
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala			
				140					145					150			
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe			
				155					160					165			
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe			
				170					175					180			
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly			
				185					190					195			
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu			
				200					205					210			
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala			
				215					220					225			
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser			
				230					235					240			
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro			
				245					250					255			
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr			
				260					265					270			
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu			
				275					280					285			
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala			
				290					295					300			
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp			
				305					310					315			
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn			
				320					325					330			
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile			
				335					340					345			
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala			
				350					355					360			
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr			

				365					370					375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
				455					460					465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
				470					475					480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
				530					535					540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly
				605					610					615
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp
				620					625					630
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
				635					640					645
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His

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Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser		
	665		670		675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val			
	680		685		690
Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr			
	695		700		705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile			
	710		715		720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val			
	725		730		735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg			
	740		745		750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val			
	755		760		765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile			
	770		775		780
Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp			
	785		790		795
Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr	Val			
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<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

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<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

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<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200

gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250

atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300

tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350

agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400

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<210> 234
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234

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				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
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Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile
				170					175					180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala
				185					190					195

Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235
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 cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
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 ctctacaat ctggaaacca tcctcccgaa gatgggcatc caaatgcct 1050
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 gtttctaaag caaccacaa ggctgtgctg gatgtcagtg aagagggcac 1150
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 gtccctctta cttcactgtc tccttcaata ggaccttcct gatgatgatt 1250
 acaataaag ccacagacgg tattctcttt ctagggaaag tggaaaatcc 1300
 cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350
 tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400
 tgaccccagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450
 aatcaccaaa ccatcaacag ggaccccagt cacaagccaa caccattaa 1500

cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550
 ggatgttgct gggttaccat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650
 attcaataaaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
 200 205 210

Lys	Trp	Glu	Lys	Pro	Phe	His	Leu	Glu	Tyr	Thr	Arg	Lys	Asn	Phe	215	220	225
Pro	Phe	Leu	Val	Gly	Glu	Gln	Val	Thr	Val	Gln	Val	Pro	Met	Met	230	235	240
His	Gln	Lys	Glu	Gln	Phe	Ala	Phe	Gly	Val	Asp	Thr	Glu	Leu	Asn	245	250	255
Cys	Phe	Val	Leu	Gln	Met	Asp	Tyr	Lys	Gly	Asp	Ala	Val	Ala	Phe	260	265	270
Phe	Val	Leu	Pro	Ser	Lys	Gly	Lys	Met	Arg	Gln	Leu	Glu	Gln	Ala	275	280	285
Leu	Ser	Ala	Arg	Thr	Leu	Ile	Lys	Trp	Ser	His	Ser	Leu	Gln	Lys	290	295	300
Arg	Trp	Ile	Glu	Val	Phe	Ile	Pro	Arg	Phe	Ser	Ile	Ser	Ala	Ser	305	310	315
Tyr	Asn	Leu	Glu	Thr	Ile	Leu	Pro	Lys	Met	Gly	Ile	Gln	Asn	Ala	320	325	330
Phe	Asp	Lys	Asn	Ala	Asp	Phe	Ser	Gly	Ile	Ala	Lys	Arg	Asp	Ser	335	340	345
Leu	Gln	Val	Ser	Lys	Ala	Thr	His	Lys	Ala	Val	Leu	Asp	Val	Ser	350	355	360
Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Lys	Phe	Ile	365	370	375
Val	Arg	Ser	Lys	Asp	Gly	Pro	Ser	Tyr	Phe	Thr	Val	Ser	Phe	Asn	380	385	390
Arg	Thr	Phe	Leu	Met	Met	Ile	Thr	Asn	Lys	Ala	Thr	Asp	Gly	Ile	395	400	405
Leu	Phe	Leu	Gly	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ser				410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100

gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200

ggaccagggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga 350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
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gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
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 tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaaccat 1900
 ggccttggtc caggccctgg agggaaatcat ggagcccccc acaggcccag 1950
 gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000
 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050
 gcattcttca ggaaggaaga gacctgggca cccaagacct gggttccttt 2100
 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150
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 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
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 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
 1 5 10 15
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75
 Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				365					370					375
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				380					385					390

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				395					400					405
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				410					415					420
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala
				425					430					435
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				440					445					450
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				455					460					465
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala
				470					475					480
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala
				485					490					495
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile
				500					505					510
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe
				515					520					525
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn
				530					535					540
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly
				545					550					555
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro
				560					565					570
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile
				575					580					585
Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro				
				590					595					

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggtcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150

ccccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caagggtgcc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650

ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700

tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750

agtcaacacg cttttcatca accttcccgc cctgtggagg agcgtcgcca 800

acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	
Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser	185	190	195	
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser	200	205	210	
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly				

215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg		
230	235	240

Ser Val Ala Asn Ile Met Pro
245

<210> 249
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 249
caatatgcat cttgcacgtc tgg 23

<210> 250
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
aagcttctct gcttcctttc ctgc 24

<210> 251
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252
<211> 3781
<212> DNA
<213> Homo sapiens

<400> 252
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cagtggacac tccaggaaga gcggccccgc ggggggagat gaccgtgcgc 100
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ggggcgagacc gcggggcgga gctgccgccc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250

ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300
 cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
 gccgcctccg acctggggcg tcagcccccg gatcagcctg cctctgggct 400
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 acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
 agaggccctc tttgcactca gtagcaacct cagcttcctg ccaggcgggg 550
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 cacccttttc tatggggtct tcacttccca gtggcacagg ggaactacag 1300
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 aacttctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550
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 gcctctacca gcctcagctg gccaccaggg cgtggatcca ggacatcgag 1950
 ggagccagcg ccaaggacct ttgcagcgcg tcttcggttg tgtccccgtc 2000
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 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
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 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu
 80 85 90
 Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr
 95 100 105
 Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys
 110 115 120

Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile	125	130	135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly	140	145	150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn	155	160	165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp	170	175	180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala	185	190	195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe	200	205	210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro	215	220	225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	230	235	240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	245	250	255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	260	265	270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	275	280	285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	290	295	300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	305	310	315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	320	325	330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	335	340	345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	350	355	360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys	365	370	375
Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	380	385	390
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	395	400	405

Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro	Asp	Arg	Val	Leu	410	415	420
Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser	425	430	435
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala	440	445	450
Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	Phe	455	460	465
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	470	475	480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	485	490	495
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	500	505	510
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	515	520	525
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	530	535	540
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	545	550	555
Tyr	Gln	Pro	Gln	Leu	Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu	560	565	570
Gly	Ala	Ser	Ala	Lys	Asp	Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser	575	580	585
Pro	Ser	Phe	Val	Pro	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln	590	595	600
Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser	605	610	615
Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	Asn	Gly	Ala	Pro	Val	Asn	620	625	630
Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	Gly	Asp	Leu	Leu	Leu	635	640	645
Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu	650	655	660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val	665	670	675
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	Val	Pro	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
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Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
				710					715					720	
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
				725					730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
				740					745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
				755					760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
				770					775					780	
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
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Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
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Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

tgaagccagg gcagcgtcct ctgg 24

<210> 256

<211> 18

<212> DNA

<213> Artificial Sequence

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 <223> unknown base

 <400> 259
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 agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

 tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200

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<210> 260
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg
				20					25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val
				245					250					255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser
				260					265					270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys

	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn Ser	Lys Ile His Gln Ala	
	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg	Leu
	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His	Arg
	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr	Ser
	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro	Pro
	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu	Glu
	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp	Gly
	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala	Leu
	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn	Ala
	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr	Gly
	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu	Asp
	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr	Val
	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys	Ile
	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala	Lys
	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn	Ser
	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser	Glu
	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro	Leu
	530	535	540
Ser Gly Arg Phe	Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
	545	550	555
Lys Thr Cys Leu	Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu

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Leu Phe Asn Ser	Asp 575	Ser Asn Pro Asp	Lys 580	Ala Lys Gln Val	Glu 585
Leu Met Arg Asp	Tyr 590	Arg Ile Lys Tyr	Pro 595	Lys Ala Asp Met	Gln 600
Ile Leu Pro Val	Ser 605	Gly Glu Phe Ser	Arg 610	Ala Leu Ala Leu	Glu 615
Val Gly Ser Ser	Gln 620	Phe Asn Asn Glu	Ser 625	Leu Leu Phe Phe	Cys 630
Asp Val Asp Leu	Val 635	Phe Thr Thr Glu	Phe 640	Leu Gln Arg Cys	Arg 645
Ala Asn Thr Val	Leu 650	Gly Gln Gln Ile	Tyr 655	Phe Pro Ile Ile	Phe 660
Ser Gln Tyr Asp	Pro 665	Lys Ile Val Tyr	Ser 670	Gly Lys Val Pro	Ser 675
Asp Asn His Phe	Ala 680	Phe Thr Gln Lys	Thr 685	Gly Phe Trp Arg	Asn 690
Tyr Gly Phe Gly	Ile 695	Thr Cys Ile Tyr	Lys 700	Gly Asp Leu Val	Arg 705
Val Gly Gly Phe	Asp 710	Val Ser Ile Gln	Gly 715	Trp Gly Leu Glu	Asp 720
Val Asp Leu Phe	Asn 725	Lys Val Val Gln	Ala 730	Gly Leu Lys Thr	Phe 735
Arg Ser Gln Glu	Val 740	Gly Val Val His	Val 745	His His Pro Val	Phe 750
Cys Asp Pro Asn	Leu 755	Asp Pro Lys Gln	Tyr 760	Lys Met Cys Leu	Gly 765
Ser Lys Ala Ser	Thr 770	Tyr Gly Ser Thr	Gln 775	Gln Leu Ala Glu	Met 780
Trp Leu Glu Lys	Asn 785	Asp Pro Ser Tyr	Ser 790	Lys Ser Ser Asn	Asn 795
Asn Gly Ser Val	Arg 800	Thr Ala			

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 262
<211> 24
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
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<210> 263
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

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tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
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gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccocatc 500
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 ataaaaatat tttctattgt agttcaaatg tgccaacatc tttatgtgtc 1350
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<210> 265
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 265
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 20 25 30
 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
 35 40 45
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser
 50 55 60
 Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys
 65 70 75
 Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu
 80 85 90

Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	95	100	105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	110	115	120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	125	130	135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	140	145	150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	155	160	165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	170	175	180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	185	190	195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	200	205	210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	215	220	225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	230	235	240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	245	250	255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	260	265	270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	275	280	285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	290	295	300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	305	310	315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	320	325	330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	335	340	345
Leu	Leu	Lys	Val	Tyr											350		

<210> 266
 <211> 2403
 <212> DNA

<213> Homo sapiens

<400> 266

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aatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcatataca cagacacaaa aattctaaat aaaattttta 2250
caaattaaac taaaacaatat atttaaagat gatataaac tactcagtgt 2300
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aaa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
  1             5             10             15

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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala
          20             25             30

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Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

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	35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe	50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser	65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp	80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr	95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile	110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly	125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile	140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg	170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile	185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu	200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu	215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu	230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile	245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys	290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro	305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val			

	320		325		330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val	335		340		345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp	350		355		360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn	365		370		375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr	380		385		390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr	395		400		405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe	410		415		420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys	425		430		435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr	440		445		450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp	455		460		465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

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 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
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tatgtgctgg ctcttagaa ggaaaaacag atgcatgcca gggatgactct 1150
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cca 2103

<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
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Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
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Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr
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Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
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Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
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Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
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Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
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Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
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<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	170	175	180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	185	190	195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	200	205	210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	215	220	225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	230	235	240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	245	250	255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	260	265	270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	275	280	285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	290	295	300
Glu	Met	Glu	Glu	Leu											305		

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<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	185	190	195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	200	205	210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	215	220	225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	230	235	240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	245	250	255
Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	260	265	270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	275	280	285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	290	295	300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	305	310	315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	320	325	330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	335	340	345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	350	355	360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	365	370	375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	380	385	390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	395	400	405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	410	415	420
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<210> 276
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 <212> DNA
 <213> Homo sapiens

<400> 276

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<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	45
				35					40						
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	60
				50					55						
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	75
				65					70						
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	90
				80					85						
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	105
				95					100						
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	120
				110					115						
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	135
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Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	150
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Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	165
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Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	180
				170					175						
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	195
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Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro	290	295	300
Phe	Asn	Val	Ile	Arg	His	Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro	305	310	315
Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val	320	325	330
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp	335	340	345
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu	350	355	360
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg	365	370	375
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr	380	385	390
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr	395	400	405
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val	410	415	420
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr	425	430	435
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly	440	445	450
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp	455	460	465
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala	470	475	480

Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala	485	490	495
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg	500	505	510
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu	515	520	525
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg	530	535	540
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser	545	550	555
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala	560	565	570
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala	575	580	585
Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala					755	760	

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
ctgctggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggctcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
agggtccctt agccgggagc agggcgcgca gccaggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100
ttccttctcc ctgggggtcct gctctcagag gctgccaaaa tcctgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450

ggatatcatg gattccttaa agaattgagaa ctctgacatg gtgatagttg 500
 aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
 tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600
 aatccccttg tcttatgttc cagtattccg ttccttgctg actgatcaca 650
 tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
 aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
 tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800
 agttgtggtt cattaactct gactttgcct ttgattttgc tcgacctctg 850
 cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900
 agtaccacaa gacttggaga acttcattgc caagtttggg gactctggtt 950
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 atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccca 1150
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 catccagcat ggtgtgcccc tgggtggggat ccctctcttt ggagaccagc 1250
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 ttaaagaagc tcaaggcaga gacattggct ctttaagatga aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcacacctg 1400
 gctcccaccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
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 gtccctgtct ctggtgccc cagtgaagctc cttcttggt gagcaggcat 2250
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 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile

				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly
				260					265					270
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
				290					295					300
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser

440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50

gggtgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
 cccgtcacac acacatacca tgttctccat cccccagggt ccagccctca 150
 gtgctgtccc atccagcagg gctaccctga agctctgggt gcagccctcc 200
 cgtccagtgg gcaggcgggt tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300
 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
 ccaggggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450
 gggttgcaga gccctcagc catgttgga gccaaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550
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 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
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 caactagaga atgggtggta gtgagacact atagaattac taaggagaag 2250
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

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ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
agccagcgct ctacaggagg acctgcgctg tcgcgcgagg ggtctgggag 300
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agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
 acctgtacca caccatgtac atggaggccc tgggtgaagct ctctgacaag 1300
 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400
 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttataa 1450
 gaaattataa caattttgct aaaccaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	

Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	260	265	270
Ala	Asp	Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	275	280	285
Lys	Gln	Val	Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln	290	295	300
Lys	Lys	Phe	Gln	Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	305	310	315
Gly	Arg	Gly	Leu	Phe	Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	320	325	330
Ser	Lys	Pro	Ile	Thr	Thr	Val	Val	Gly	Glu	Pro	Ile	Thr	Ile	Pro	335	340	345
Lys	Leu	Glu	His	Pro	Thr	Gln	Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr	350	355	360
Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu	Phe	Asp	Lys	His	Lys	Thr	365	370	375
Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu	Glu	Val	Asn			380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggcggcggg atggggggccg ggggcggcgg gcgcgcgact cgctgaggcc 50
ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100
cggggcccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggctctg cacggagtgt aactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcggc tggacgtggt actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggctgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgagagg 800

ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850
 gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaagg 900
 cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
 atgtaaccct gaacttcaga ggaaacaaga acccgtccct gctggggatc 1000
 ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttcctct 1050
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 tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcatg 1150
 tttccagggg agcagtttaa gcctgcccg aggccgtgga ccctcctgaa 1200
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 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150
 ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gccgcctca 2200
 gcctcccaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250

atttcttttt aaggctgaat gatgggggcc aggcacgatg gctcacgcct 2300
 gtgatcccaa gtagcttgga ttgtaaacad gcaccacat gcctggctaa 2350
 tttttgtatt tttagtagag acgtgttagc caggctggtc tcgatctcct 2400
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 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600
 ttgttctgtt gcccaggctg gagtacagtg gcacagtctt ggctcactgc 2650
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 agctgtattt ttttgtattt tgtattttgt agctgtagtt tttgtatttt 2750
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 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccctaacta 2950
 ccagggagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
				350					355					360					
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
 cttcctctgt gggtaggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
 gccacctcca tgctaacgcg g 21

<210> 300
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 300
 ccaaggtcct cgctaagaag gagctgctct acgtgcccct catcg 45

<210> 301
 <211> 1334
 <212> DNA
 <213> Homo sapiens

<400> 301
 gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50
 tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
 tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150
 tcagtttgtc ttgtgggggtt ggtggcaggc aggccggctt acgcctgata 200
 cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
 tagctggggg ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
 ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
 tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
 ctggcctgac agaattctcat cttgttttaat gctctcataa gaccacttgt 650
 ttcccttttg cagcacttgc cactcagttg tatcttttatg tgcgtttgtg 700
 gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750
 agggtaagg gcattgctgt gcctgccagg tatagtgcct acatgtgggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900
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 tctgtactaa aaatacacaa attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggagggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggaggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
 1 5 10 15
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
 20 25 30
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp

	65		70		75									
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
			80						85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
			95						100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
			110						115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
			125						130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							
			140											

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100
 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattggc tcagtgttgg cccaggaggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250
 tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaa at gatctccaag ggcccttata ccccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450
 taagaatcag ttattgccgg gtgtgggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgagggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1				5				10						15
Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20				25						30
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35				40						45
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55						60
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro

				65						70					75
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala	
				80					85					90	
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly	
				95					100					105	
Arg	Arg	Arg	Asp												

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305
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 tgtcactgcc tcccgccgcc tcctgcccgc gccatgaccc agccggtgcc 100
 ccggtctctc gtgcccgcgc cgctggccct gggctcagcc gcactgggcg 150
 ccgccttcgc cactggcctc ttcttgggga ggcggtgccc cccatggcga 200
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
 caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc 400
 gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450
 cgctgcccgc ggacggggcg gtggtgacct gcgaggtgga cgcgcagccc 500
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550
 cgacctccgg ctgaagcccg ccttggagac cctggacgag ctgctggcgg 600
 cgggcgaggc cggcaccttc gacgtggccg tgggtggatgc ggacaaggag 650
 aactgctccg cctactacga gcgctgcctg cagctgctgc gaccgaggag 700
 catcctcgcc gtccctcagag tcctgtggcg cgggaagggtg ctgcaacctc 750
 cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcata 800
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850
 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
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 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
				65					70					75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
				80					85					90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
				95					100					105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
				110					115					120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
				125					130					135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
				140					145					150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
				155					160					165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
				170					175					180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
				185					190					195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
				200					205					210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
				215					220					225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
				230					235					240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
				245					250					255

Leu Thr Leu Ala Phe Lys Ile
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<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
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ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250
aatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350
cgccagtgag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
ggcagtgacg ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
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agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150
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aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
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actataaacg gttttttaat ga 2272

<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308
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20 25 30
Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

	35		40		45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro	50		55		60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys	65		70		75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala	80		85		90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala	95		100		105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp	110		115		120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala	125		130		135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser	140		145		150
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser	155		160		165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala	170		175		180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu	185		190		195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala	200		205		210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys	215		220		225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser	230		235		240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser	245		250		255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val	260		265		270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro	275		280		285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser	290		295		300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu	305		310		315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg					

				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
				365					370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
				380					385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
				395					400					405
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
				410					415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
				425					430					435
Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr
				440					445					450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys
				455					460					465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser
				470					475					480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg
				485					490					495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser
				500					505					510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys
				515					520					525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala
				530					535					540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile
				545					550					555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys
				560					565					570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala
				575					580					585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala
				590					595					600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu

	605		610		615
Asp Lys Glu His	Glu Glu Gly Arg Asp	Ser Glu Glu Gly Pro	Arg		
	620		625		630
Cys Gly Ser Ser	Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro			
	635		640		645
Asp Leu Asp Arg	Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg	Ala		
	650		655		660
Arg Gly Asp Ser	Glu Ala Leu Asp Glu	Glu Ser			
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<210> 309
 <211> 3871
 <212> DNA
 <213> Homo sapiens

<400> 309
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 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250
 taaaagact tgctgctttc aaatagctgt attccctttt tgggttcatc 300
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350
 tgctcttggg agccaaagac cacatctttc tactcagtct ggttgactta 400
 aaaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450
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 tcagagtact tcagccctat aaaaaactc acatatatgt gtgtggaact 550
 ggagcatttc atccaatatg tgggtatatt gatcttgag tctacaagga 600
 ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650
 aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700
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 tgaatcatct caagaaggca gtacctccga taaaaccatc ctttctcgag 950

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 ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150
 agctccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200
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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	His	Leu	Phe	Pro	Ala	Leu	Met	Met	Leu	Ser	Met	Thr	Met	Leu
				20					25					30

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75

Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile
				80					85					90

Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105

Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120

Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135

Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150

Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165

Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180

Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195

Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210

Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225

His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	230		235		240
Ala Lys Phe Ile	Gly Thr Phe Phe Ile	Pro Asp Thr Tyr Asn	Pro		
	245	250		255	
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Arg Glu Ser Ser Gln	Glu		
	260	265		270	
Gly Ser Thr Ser	Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg	Val		
	275	280		285	
Cys Lys Asn Asp	Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys	Trp		
	290	295		300	
Thr Thr Phe Leu	Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly	Ser		
	305	310		315	
Asp Gly Ala Asp	Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr	Leu		
	320	325		330	
Leu Pro Thr Arg	Asp Glu Arg Asn Pro	Val Val Tyr Gly Val	Phe		
	335	340		345	
Thr Thr Thr Ser	Ser Ile Phe Lys Gly	Ser Ala Val Cys Val	Tyr		
	350	355		360	
Ser Met Ala Asp	Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala	His		
	365	370		375	
Lys Glu Ser Ala	Asp His Arg Trp Val	Gln Tyr Asp Gly Arg	Ile		
	380	385		390	
Pro Tyr Pro Arg	Pro Gly Thr Cys Pro	Ser Lys Thr Tyr Asp	Pro		
	395	400		405	
Leu Ile Lys Ser	Thr Arg Asp Phe Pro	Asp Asp Val Ile Ser	Phe		
	410	415		420	
Ile Lys Arg His	Ser Val Met Tyr Lys	Ser Val Tyr Pro Val	Ala		
	425	430		435	
Gly Gly Pro Thr	Phe Lys Arg Ile Asn	Val Asp Tyr Arg Leu	Thr		
	440	445		450	
Gln Ile Val Val	Asp His Val Ile Ala	Glu Asp Gly Gln Tyr	Asp		
	455	460		465	
Val Met Phe Leu	Gly Thr Asp Ile Gly	Thr Val Leu Lys Val	Val		
	470	475		480	
Ser Ile Ser Lys	Glu Lys Trp Asn Met	Glu Glu Val Val Leu	Glu		
	485	490		495	
Glu Leu Gln Ile	Phe Lys His Ser Ser	Ile Ile Leu Asn Met	Glu		
	500	505		510	
Leu Ser Leu Lys	Gln Gln Gln Leu Tyr	Ile Gly Ser Arg Asp	Gly		

515					520					525				
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala
				530					535					540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp
				545					550					555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala
				560					565					570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp
				575					580					585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val
				590					595					600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro
				605					610					615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly
				620					625					630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys
				635					640					645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser
				650					655					660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr
				665					670					675
Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu
				680					685					690
Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu
				695					700					705
Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu
				710					715					720
Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp
				725					730					735
His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp
				740					745					750
Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His
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<211> 25

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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 <210> 312
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 312
 gcttggacat gtaccaggcc gtgg 24

 <210> 313
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 313
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 <210> 314
 <211> 3934
 <212> DNA
 <213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu
				20					25					30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala
				35					40					45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg
				50					55					60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu
				65					70					75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala
				80					85					90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
				95					100					105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp
				110					115					120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
				125					130					135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
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Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	305	310	315
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly	320	325	330
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	335	340	345
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	350	355	360
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
				35					40					45	
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	
				50					55					60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	
				65					70					75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	
				80					85					90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	
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Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	
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Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	
				125					130					135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu	
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				170					175					180	
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn	
				185					190					195	
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala	
				200					205					210	
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val	
				215					220					225	
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg	
				230					235					240	
Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His	

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Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu	
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Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu	
				320					325					330	
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys	
				335					340					345	
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala	
				350					355					360	
His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys	
				365					370					375	
Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val	
				380					385					390	
Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser	
				395					400					405	
Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr	
				410					415					420	
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro	
				425					430					435	
Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln	
				440					445					450	
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro	
				455					460					465	
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala	
				470					475					480	
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys	
				485					490					495	
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp	
				500					505					510	
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro	
				515					520					525	
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	

530										535				540			
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly			
				545					550					555			
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn			
				560					565					570			
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu			
				575					580					585			
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe			
				590					595					600			
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro			
				605					610					615			
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr			
				620					625					630			
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser			
				635					640					645			
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala			
				650					655					660			
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys			
				665					670					675			
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly			
				680					685					690			
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile			
				695					700					705			
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro			
				710					715					720			
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser			
				725					730					735			
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp			
				740					745					750			
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr			
				755					760					765			
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro			
				770					775					780			
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg			
				785					790					795			
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro			
				800					805					810			
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu			

	815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys			
	830	835	

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 320
 ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
 <211> 1197
 <212> DNA
 <213> Homo sapiens

<400> 321
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 gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
 ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
 ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgtttt 200
 gggggagcaa gcacttctgg ccggagggtac ccaaaaaagc ctatgacatg 250
 gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
 tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
 aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
 gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650
 actttgagga ggaggagaa gatcttcact ttctgcca cgaaaaaaaa 700
 gggattgaac aaaatgaaca gtgggtgggc cctcaagtga aagtagagaa 750
 gaccggtcac gccagacaag caagtgagga agaactcca ataaatgact 800
 atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850
 tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
 acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
 tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
 gggaggggtct aataggaggt ttgagctcaa atgcttaa ac tgctggcaac 1050
 atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100
 ccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
 tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

	80	85	90
Arg Ser Gly Asn Gly Thr Asp Glu Thr	Leu Glu Val His Asp Phe		
95	100	105	
Lys Asn Gly Tyr Thr Gly Ile Tyr Phe	Val Gly Leu Gln Lys Cys		
110	115	120	
Phe Ile Lys Thr Gln Ile Lys Val Ile	Pro Glu Phe Ser Glu Pro		
125	130	135	
Glu Glu Glu Ile Asp Glu Asn Glu Glu	Ile Thr Thr Thr Phe Phe		
140	145	150	
Glu Gln Ser Val Ile Trp Val Pro Ala	Glu Lys Pro Ile Glu Asn		
155	160	165	
Arg Asp Phe Leu Lys Asn Ser Lys Ile	Leu Glu Ile Cys Asp Asn		
170	175	180	
Val Thr Met Tyr Trp Ile Asn Pro Thr	Leu Ile Ser Val Ser Glu		
185	190	195	
Leu Gln Asp Phe Glu Glu Glu Gly Glu	Asp Leu His Phe Pro Ala		
200	205	210	
Asn Glu Lys Lys Gly Ile Glu Gln Asn	Glu Gln Trp Val Val Pro		
215	220	225	
Gln Val Lys Val Glu Lys Thr Arg His	Ala Arg Gln Ala Ser Glu		
230	235	240	
Glu Glu Leu Pro Ile Asn Asp Tyr Thr	Glu Asn Gly Ile Glu Phe		
245	250	255	
Asp Pro Met Leu Asp Glu Arg Gly Tyr	Cys Cys Ile Tyr Cys Arg		
260	265	270	
Arg Gly Asn Arg Tyr Cys Arg Arg Val	Cys Glu Pro Leu Leu Gly		
275	280	285	
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln	Gly Gly Arg Val Ile Cys		
290	295	300	
Arg Val Ile Met Pro Cys Asn Trp Trp	Val Ala Arg Met Leu Gly		
305	310	315	

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtcctacctg aaagggtctt ggatggagtg 250
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
tggcgctgcc ccaagacctc caggctgcc gcgcctcat ggtcatctcc 350
tgctgctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
cacgcgtgc gccaaaggca caccgccta gaccacctt gccatcctcg 450
gcggcacct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
tggaccacca acgacgtggt gcagaacttc tacaaccgc tgctgccag 550
cgcatgaag tttagattg gccaggcct gtacctgggc ttcattctct 600
cgctccctct gctcattggt ggcacctgc tttgcctgtc ctgccaggac 650
gaggcacct acaggcccta ccaggccccg cccaggggca ccacgaccac 700
tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
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ataccaaaga ctgaaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
atatattatg gggtgatttg ataacaagtt taatataaag tgacttgga 1100
gtttggctcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
1				5					10					15

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200

aaccccggtca cctccgtggt ccagtagcaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350
gtcctgggtg ccattggcct cctgggtatcc atctttgccc tgaaatgcat 400
ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
gtgtttgcca acatgctggg gactaacttc tggatgtcca cagctaaca 550
gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600
ttgggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
gggggtgtga tgatgtgcat cgctgcccgg ggctggcac cagaagaaac 700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta 850
tccttccaag cagactatg tgtaatgctc taagacctt cagcacgggc 900
ggaagaaact ccggagagc tcacccaaaa aacaaggaga tcccatctag 950
atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
atcttcaatc ctctatttct ttttttaaat ataactttct actctgatga 1150
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
ccccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250
tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450
agtcattttc agtttgaggc aaccaaact ttctactgct gttgacatct 1500
tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600

atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155					160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170					175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245					250					255
Ser	Lys	His	Asp	Tyr	Val									
				260										

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tggtggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350
 tgctgcttcc gtgatgtcct tcttggtctt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
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 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650

tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaattctt aattacagga 900
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgctttttcag ggaaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaaca aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800
 atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgtttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328

<211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val	215	220	225	

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329

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 gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150
 gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgctgggtgc tcacctctgg gattgtcttt gtcactctcag gggtcctgac 400
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
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 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
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 gagccatcca gaagtggcag tgcccaacag ctttgggatg gggtcgtacc 750
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 tctggatctt gacatgcca tcttagaagc cagtcaagct atggaactaa 950
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 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atcctactca ggtctctgga gctcctctct tcaccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250
 gccccctcg tctaccccc ttacactca catttttatc aaataaagca 1300
 tgttttgtta gtgca 1315

<210> 330
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu	
1				5					10					15	
Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp	
				20					25					30	
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val	
				35					40					45	
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly	
				50					55					60	
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val	
				80					85					90	
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr	
				95					100					105	
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr	
				110					115					120	
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro	
				125					130					135	
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	
				140					145					150	
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr	
				155					160					165	
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu	
				170					175					180	
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His	
				185					190					195	
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly	
				200					205					210	
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val						
				215					220						

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
 gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggg 200
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
 ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
 gcaagttcta tagctccttg ttggctctcc cgcctgcctt ggaaacagcc 350
 cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
 tggcatctgt ggcatagaag aggtccagtg cacaggctct aacgagaggg 450
 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
 atcttcgttc tgattccggt gagctggaca gccaatataa tcatacagaga 550
 tttctacaac ccagccatcc acatagggtc gaaacgagag ctgggagcag 600
 cacttttcct tggctgggca agcgtgctg tcctcttcat tggagggggg 650
 ctgctttgtg gatattgctg ctgcaacaga aagaagcaag ggtacagata 700
 tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
 caatgcttag taagacctcc accagttatg tctaattgct ccttttggct 800
 ccaagtatgg actatgggtc atgtttttta taaagtctg ctagaaactg 850
 taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
 cgaaagtttc aatttggtac tgggtggtagg aatgaaaatg acttacttgg 950
 acattctgac ttcaggtgta ttaaattgcat tgactattgt tggacccaat 1000
 cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050
 caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
 ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
 acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
				20					25					30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

	35		40		45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn					
	50		55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe					
	65		70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala					
	80		85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly					
	95		100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser					
	110		115		120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys					
	125		130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly					
	140		145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu					
	155		160		165
Ser Lys Thr Ser Thr Ser Tyr Val					
	170				

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
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ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
ggtagggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450
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tttttaacac gtcaataaaa aaataatctc ccaga 535

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<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
 1 5 10 15
 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75
 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 335
 cccgcgcccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50
 ctgctcgcgc cccgcgcgcca tggctgcctc cccgcgcgcg cctgctgtcc 100
 tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
 ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200
 tgttccaact aagactaaag tggccggtga tgagaataaa gccaaagaat 250
 tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
 cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
 agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400
 gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
 gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
 ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550
 agcgattctc ttcattgtat tctaatgcc ttacactact tggtttctga 600
 tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttaa aacaacacat gtaaattgct tttgatattt catgggaatg 700

cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly	
1				5					10					15	
Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser	
				20					25					30	
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val	
				35					40					45	
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu	
				50					55					60	
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg	
				65					70					75	
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met	
				80					85					90	
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu	
				95					100					105	
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln	
				110					115					120	
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr	
				125					130					135	
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr			
				140					145						

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150

ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

ccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcggtccc ccaaatcccc cctgccccgc ggggtccgag 650
cccggcccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
tccccctgac cgccactctg ggccctggccg gcttcaccct gctcctcagt 800
ctcctggcct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850
agcgtcgccg gcccctccgg accttgctcc ccgcgcgcg gcgggagctg 900
ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
gcccagccct gcgccgcaga ggactcccgg gactggcgga ggccccgccc 1000
tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
cgcactggga gtgggctcct cggggctcggg catctgctgt cgctgcctcg 1100
gccccgggca gagccggggc gccccggggg cccgtcttag tgttctgccg 1150
gaggaccag ccgcctccaa tccctgacag ctccctgggc tgagttgggg 1200
acgccaggtc ggtgggaggc tgggtgaagg gagcggggag gggcagagga 1250
gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
aaaaaaaaa 1310

<210> 338
<211> 246
<212> PRT
<213> Homo sapiens

<400> 338
Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
1 5 10 15
Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
20 25 30
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
tcttggcttc ctcttactc ccactctggac ccagtcccct ggttcctgtc 800
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
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Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
20 25 30
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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actgagaacc caccagctca tcccagacac ctcatagcaa cctatattata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
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ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250

atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300
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<210> 347

<211> 639

<212> PRT
 <213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	1	5	10	15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	20	25	30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	35	40	45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	50	55	60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	65	70	75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	80	85	90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	95	100	105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	110	115	120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	125	130	135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	140	145	150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	155	160	165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	170	175	180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	185	190	195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	200	205	210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	215	220	225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	230	235	240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	245	250	255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	260	265	270	

Ala	Thr	Arg	Ala	Thr	Gly	Asp	Val	Leu	Val	Phe	Met	Asp	Ala	His	275	280	285
Cys	Glu	Cys	His	Pro	Gly	Trp	Leu	Glu	Pro	Leu	Leu	Ser	Arg	Ile	290	295	300
Ala	Gly	Asp	Arg	Ser	Arg	Val	Val	Ser	Pro	Val	Ile	Asp	Val	Ile	305	310	315
Asp	Trp	Lys	Thr	Phe	Gln	Tyr	Tyr	Pro	Ser	Lys	Asp	Leu	Gln	Arg	320	325	330
Gly	Val	Leu	Asp	Trp	Lys	Leu	Asp	Phe	His	Trp	Glu	Pro	Leu	Pro	335	340	345
Glu	His	Val	Arg	Lys	Ala	Leu	Gln	Ser	Pro	Ile	Ser	Pro	Ile	Arg	350	355	360
Ser	Pro	Val	Val	Pro	Gly	Glu	Val	Val	Ala	Met	Asp	Arg	His	Tyr	365	370	375
Phe	Gln	Asn	Thr	Gly	Ala	Tyr	Asp	Ser	Leu	Met	Ser	Leu	Arg	Gly	380	385	390
Gly	Glu	Asn	Leu	Glu	Leu	Ser	Phe	Lys	Ala	Trp	Leu	Cys	Gly	Gly	395	400	405
Ser	Val	Glu	Ile	Leu	Pro	Cys	Ser	Arg	Val	Gly	His	Ile	Tyr	Gln	410	415	420
Asn	Gln	Asp	Ser	His	Ser	Pro	Leu	Asp	Gln	Glu	Ala	Thr	Leu	Arg	425	430	435
Asn	Arg	Val	Arg	Ile	Ala	Glu	Thr	Trp	Leu	Gly	Ser	Phe	Lys	Glu	440	445	450
Thr	Phe	Tyr	Lys	His	Ser	Pro	Glu	Ala	Phe	Ser	Leu	Ser	Lys	Ala	455	460	465
Glu	Lys	Pro	Asp	Cys	Met	Glu	Arg	Leu	Gln	Leu	Gln	Arg	Arg	Leu	470	475	480
Gly	Cys	Arg	Thr	Phe	His	Trp	Phe	Leu	Ala	Asn	Val	Tyr	Pro	Glu	485	490	495
Leu	Tyr	Pro	Ser	Glu	Pro	Arg	Pro	Ser	Phe	Ser	Gly	Lys	Leu	His	500	505	510
Asn	Thr	Gly	Leu	Gly	Leu	Cys	Ala	Asp	Cys	Gln	Ala	Glu	Gly	Asp	515	520	525
Ile	Leu	Gly	Cys	Pro	Met	Val	Leu	Ala	Pro	Cys	Ser	Asp	Ser	Arg	530	535	540
Gln	Gln	Gln	Tyr	Leu	Gln	His	Thr	Ser	Arg	Lys	Glu	Ile	His	Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val	
				560					565					570	
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln	
				575					580					585	
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser	
				590					595					600	
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu	
				605					610					615	
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe	
				620					625					630	
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg							
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<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351

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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatect cccctcgaac ccaccagcc ccagcccgcc ccccggtgtgc 200
caggggaggg cctcgggcc cagtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctect cgggtcccaa gatcacgtcg gcaagtcctg 300
cctggcactg cccccccagc cccccatca ggctttgagg agggggccgcc 350
ctcatcccaa taccctggg ctatcgtgtg gggtcaccac gtgtctcgag 400
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gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
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tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
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 gccccaccg tcgcccagg acccgaggac agcaccgcgc aggagcggct 300
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 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
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Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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 gttggccggc ggcgggcccg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggggat ttccccaacg agctgcgaaa 400
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 acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
 agcctagcac ctgaaggatc aatgccatca cccgcggggg acctccccta 550
 agtagccccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600
 tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
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 acccgtgcca gggccctact gtccctgggg tcccaggctc tccttggagg 850
 gggctccccg ccttccacct ggctgtcatc gggtagggcg gggccgtggg 900
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 tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000
 gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln				

	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150
Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357
 <211> 1536
 <212> DNA
 <213> Homo sapiens

<400> 357
 agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatggt 50
 cctcttatttt ctcttcacgt gtgagctggc tgcagaagtt gctgcagaag 100
 ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150
 acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
 cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
 gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
 gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
 cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
 tcagattcat ctcttcctga taatgaacaa ggcctcccca gagtatgaag 550
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
 ctctttattc tgggtggacag tggatatgaaa gaaaatggga aggtgatatc 650
 atttttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
 ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
 catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
 ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
 aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
 acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
 gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
 tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200
 ctagagaaag attgttccaa tttgtcatTT aatatcaagt ttgtatactg 1250
 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
 tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400
 cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 358
 Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
 1 5 10 15
 Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
 20 25 30
 Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
 35 40 45
 Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
 50 55 60
 Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
 65 70 75
 His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
 80 85 90
 Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
 95 100 105
 Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
 110 115 120
 Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
 125 130 135
 Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
 140 145 150
 Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
 155 160 165

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagcaa 100
cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggctcgt gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgcctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
 ccttttaatc taagggtta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattgg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggctact tcattctgga cacagttgga 1700
 tcaataactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95					100					105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
				260					265					

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100
 ccatcagcgc gccgggctgc cgctctcgg ccacggctgg gtcggggggcc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
 agaccccggc gccgccttgc tccaggtgct tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

agtgggttgga gtttctgtag atggaaaaga agtctgggtca gaaggtttag 450
 gttatgctga tgttgagaac cgtgtacat gtaaaccaga gacagttatg 500
 cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccatTT aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaatttatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu	
				65					70					75	
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro	
				80					85					90	
Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	
				95					100					105	
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	
				110					115					120	
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	
				125					130					135	
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	
				140					145					150	
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	
				155					160					165	
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	
				170					175					180	
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	
				185					190					195	
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	
				200					205					210	
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	
				215					220					225	
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	
				230					235					240	
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	
				245					250					255	
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	
				260					265					270	
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	
				275					280					285	
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	
				290					295					300	
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	
				305					310					315	
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	
				320					325					330	
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	
				335					340					345	

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagaa gtctggtcag aaggtttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttggtt cattctcctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggg gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggcc gggactgggt cgcgaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
 tcactgctct ggaaccagca ggatgggtacc ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctgggt gctatgtctc ctcccttgtc cctgcgtgct ccctgggtgga 500
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtgggcgt gtcggtgggt acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcttg 700
 agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750
 ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgta ttcagaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200
ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggacttct atcaggtcta ctctctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggctcgcaaga attcttgtgt 450
cctctttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggctgggtat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgcgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgcccctga gctgtaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtgggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagttcc 1650
 ctctgtgtta ctcccattta gaaaataaac actttttaaat gatcaaaaaa 1700
 aaaaaa 1706

<210> 374
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 374
 Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
 1 5 10 15
 Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
 20 25 30
 Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
 35 40 45
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
 50 55 60
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
 65 70 75
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
 80 85 90
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
 95 100 105
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
 110 115 120
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
 125 130 135
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
 140 145 150
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
 155 160 165
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
 170 175 180
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
 185 190 195
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
 200 205 210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	215	220	225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	230	235	240
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

<210> 375
 <211> 1098
 <212> DNA
 <213> Homo sapiens

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tgggtccccg cgcgcggggc tgggtgttgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcg cccacggcctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatctttcac acaaggtag agcagattca 250
 ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacgggt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggtgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
 gacggctaca tgatccgccc ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
 cccagggcc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggtt tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccagggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10					15	

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25					30	

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377
 <211> 496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccaggg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15

Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
				20					25					30

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
				35					40					45

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
				50					55					60

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
				65					70					75

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
				80					85					90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
				95					100					105

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
				110					115	

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt ctttctggat gggggcccag ggggccagg agagtataaa 50
ggcgatgtgg aggggtgccg gcacaaccag acgccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgetgctgct cacgcttgcc 150
ctcctggggg gcccacactg ggcaggggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctgggtgaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatatggc atgtacacca gcaaggaccg ctatttctat 450
tttgggaagc ttgatggcca gatctcctct gcctacccca gccaaagagg 500
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcataaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggatatgggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly 30
 20
 Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr 45
 35
 Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln 60
 50
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly 75
 65
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr 90
 80
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met 105
 95
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly 120
 110
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val 135
 125
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly 150
 140
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro 165
 155
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg 175
 170

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
 tgtcagcgag ccctgactca ctacagtga gctgacagg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
aaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tatatctgct gggtgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag 1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
cagaaccttt acttgcagtg gaataaaatc agtgtcatag gacagaccat 1250
gtcctggacc tggagctcct taaaaggct tgatttatca ggcaatgaga 1300
tcgaagcttt cagtggaccc agtggtttcc agtgtgtccc gaatctgcag 1350
cgctcaacc tggattccaa caagctcaca ttattgggc aagagatttt 1400
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
aatgcagcag aaatatattgc tcccttgtaa actggctgaa aagtttttaa 1500
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
ccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700
ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750
tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800
ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900

aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100
 ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150
 tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcatt 2200
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala
1				5					10					15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
				20					25					30
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
				35					40					45
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
				50					55					60
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
				65					70					75
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
				80					85					90
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
				95					100					105
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
				110					115					120
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
				125					130					135
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
				140					145					150

Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	
				155					160					165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	
				170					175					180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	
				185					190					195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	
				200					205					210	
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	
				215					220					225	
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	
				230					235					240	
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	
				245					250					255	
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	
				260					265					270	
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	
				275					280					285	
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	
				290					295					300	
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	
				305					310					315	
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	
				320					325					330	
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	
				335					340					345	
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	
				350					355					360	
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	
				365					370					375	
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	
				380					385					390	
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	
				395					400					405	
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	
				410					415					420	
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	
				425					430					435	

Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440					445					450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455					460					465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470					475					480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485					490					495
Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttgggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaata tataatgacc 200
 aacaccctaa tggctggtat atctggatcc tcctgctgct gggttttggtg 250
 gcagctcttc tctgtggagc tgtggctcctc tgcctccagt gctggctgag 300
 gagaccccgga attgattctc acaggcgcac catggcagtt tttgctggtg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactggt 400
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcctgctcc 450
 atgttttggc cctttaggct cccacacctc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaattgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttta actctttcct agcatggggg ccataaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tggtgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
 1 5 10 15
 Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
 20 25 30
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
 35 40 45
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
 50 55 60
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
 65 70 75
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
 80 85 90
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
 95 100 105
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
 110 115 120
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
 125 130 135
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
 140 145

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacccggc gtttctccag ctcgatctgg aggetgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatTTggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
atTTtgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttgggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950

aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aatttttaaag ttatttggtt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100
aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaac actgaaaac atggattcat ttctataaca catttattta 1200
agtatataac acgttttttg gacaagtga gaatgttta tcattctgtc 1250
atttgttctc aatagatgta actgtagac tacggctatt tgaaaaaatg 1300
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
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aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700
catatttggg ttaattttgc ttttattata ttggtctagg aggaagggac 1750
tttggagaat ggaactcttg aggacttttag ccagggtgtat ataataaagg 1800
tacttttgtg ctgcattaaa ttgcttgga agtgtaaca ttatattata 1850
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
accctaactt tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
atttcccttg tagcaaactt aattgccaca tgggtgcccta tatttcatag 2100
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
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acctttatgt gaagaaatta attatatgcc attgccagg 2340

<210> 395

<211> 140
 <212> PRT
 <213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10					15
Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25					30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40					45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130					135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396

cgcgccggg cgcgcggggt gagcgtgccg aggcggctgt ggcgcaggct 50
 tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100
 gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgagggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcaccactg ccttctcccg ccttcgctac ctggagtgcg 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
 acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600
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 ggcttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800
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 aacagactgc tgtcctgggc tgccctcaggt cccgagtaac ttatgttcaa 1200
 tgtgccaaca ccagtgggga gcccgcaggc ctatgtggca gcgtcaccac 1250
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 gcaaagtctc acccctttgt ctacgttgct tccccaaacc atgagcagag 1350
 ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400
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 gggcagaggg tgggtgggac ccctgctgc agggcagagt tcaggccac 1500
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 aagccccacc ctccccgcct gggctcccct tgctgcctt gcctgttccc 1850

cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950
ttcggagcct ctggaagctt agggcacatt ggttccagcc tagccagttt 2000
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aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500
ccccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccatcatc 2550
tatctaaccg gtccttgatt taataaacac tataaaagggt ttaaaaaaaaa 2600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397
Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
20 25 30
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
35 40 45
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
50 55 60
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
65 70 75
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
80 85 90

Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser	95	100	105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	110	115	120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	125	130	135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	140	145	150
Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	155	160	165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly	170	175	180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg	185	190	195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu	200	205	210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe	215	220	225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln	230	235	240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly	245	250	255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala	260	265	270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	275	280	285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	290	295	300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	305	310	315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	320	325	330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	335	340	345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu								350		

<210> 398
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagact acgttggctt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600
 tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatatttaa 650
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 ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750
 atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcacgac cccaaaccac catctcttta ctgtactagt 1000
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 ctttaaaaaa attcacagat tatatttata acctgactag agcaggatgat 1250
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 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 402
 Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
 1 5 10 15
 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
 20 25 30
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
 35 40 45

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagcttttg caaggagtga 300
caccgcocat ttacagacac gtagtgtatt ctggaggctc aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattgaa 500
ggaaaaagga aactggaagg aaaacattg cgatttcgtg gtgtacatca 550
tgcatTTgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgaccc cttggtcaat ggtgttcttg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln	1	5	10	15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	20	25	30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	35	40	45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	50	55	60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	65	70	75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	80	85	90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	95	100	105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	110	115	120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	125	130	135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	140	145	150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	155	160	165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	170	175	180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	185	190	195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	200	205	210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	215	220	225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	230	235	240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	245	250	255	

Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr
				260					265					270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly
				275					280					285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met
				290					295					300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg
				305					310					315
Glu	Met	Ser	Gly	Val	Ser	Pro	Phe							
				320										

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc ggcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
 ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggatgcatat 500
 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550
 tgcacttata ttttttagca ctctgatcta caaatgttga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag gggtacatca 900
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacgggtg 950
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgcagt gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 413

atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttcgcctcct ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag ccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaacct 1150
tcccacagca catcctacct ggaagaccag cctcagaggg tccttctgga 1200

accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
<211> 224
<212> PRT
<213> Homo sapiens

<400> 415
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
1 5 10 15
Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
20 25 30
Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
35 40 45
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
50 55 60
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
65 70 75
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
80 85 90
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
95 100 105
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
110 115 120
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
125 130 135
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
140 145 150
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
155 160 165
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
170 175 180
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
185 190 195
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
200 205 210
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
215 220

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
attctctcca cagacagctg gttc 24

<210> 421

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
gtacaagtgt ggccatcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttggttct ccgccctcct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccttgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gaggtaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
 cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgtaggaat cttgggttggc tgtctctgcc ttctcctggc tgtttatttc 1200
 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
 catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
 ggggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
 ccttccccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
 gaaatcgctg tgttgttaat gcagaganca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgcgg gatctctcct taggataaag agttgctggt 1650
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700

t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1 5 10 15
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu
 80 85 90

Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala	95	100	105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly	110	115	120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His	125	130	135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala	140	145	150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu	155	160	165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His	170	175	180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro	185	190	195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe	200	205	210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val	215	220	225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln	230	235	240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro	245	250	255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn	260	265	270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr	275	280	285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly	290	295	300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile	305	310	315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser	320	325	330
Ala	Gln	Ala	Thr	Thr	Glu	Ala									335		

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 424
 gtaaagtcgc tggccagc 18

 <210> 425
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 425
 cccgatctgc ctgctgta 18

 <210> 426
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 426
 ctgcactgta tggccattat tgtg 24

 <210> 427
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 427
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

 <210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

 <400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150
 aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350
 gggttgaatg tacaacagca actgcacca catgtgttac caatTTTTgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatcctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75
 Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
 80 85 90
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

				95						100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
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 cggagcgcgg cggagccaga cgctgaccac gtctctctcc tcggtctcct 100
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgcgcg ctccccgcag cggtcccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctgggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt taaaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650
 attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcacttaaatt gacattttta atagttttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgттаagaat tttttttata tctgttaaatt aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
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1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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Leu Pro Lys

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 432

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<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

cgcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

atgacgctcg tccaaggcca c 21

<210> 435
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 <400> 435
 cccacctgta ccacatgt 19

 <210> 436
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 <400> 436
 actccaggca ccatctgttc tccc 24

 <210> 437
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 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
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 <212> DNA
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 <400> 438
 tgacctggca aaggaagaa 19

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 cagccaccct ccagtccaag g 21

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 ctggcaggag ttaaagttcc aaga 24

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 <400> 444
 aaaggacacc gggatgtg 18

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<400> 445
agcgtacact ctctccaggc aaccag 26

<210> 446
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<400> 446
caattctgga tgaggtggta ga 22

<210> 447
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caggactgag cgcttggtta 20

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caaagcgcca agtaccggac c 21

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ccagacctca gccaggaa 18

<210> 450
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 <212> DNA
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 <400> 451
 tctgacaagc agttttctga atc 23
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 <211> 26
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 <213> Artificial Sequence
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 ctctccccct cccttttcct ttgttt 26
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 <211> 18
 <212> DNA
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 <210> 455
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 caggaaatct ggaaacctac agt 23

<210> 456
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<400> 456
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<210> 457
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<400> 457
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<210> 459
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<400> 459
 aacagcaggt gcgactcatc ta 22

<210> 460
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 tgctaggcga cgacacccag acc 23

<210> 461
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tggacacgtg gcagtgga 18

<210> 462
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<212> DNA
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<220>
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<400> 462
tcatggtctc gtcccatc 19

<210> 463
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 463
caccatttgt ttctctgtct ccccatc 27

<210> 464
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<212> DNA
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<220>
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<400> 464
ccggcatcct tggagtag 18

<210> 465
<211> 20
<212> DNA
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<220>
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<400> 465
tccccattag cacaggagta 20

<210> 466

<211> 23
 <212> DNA
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 <210> 467
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 <400> 467
 gccagagtc ccacttgt 18

 <210> 468
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 <212> DNA
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 <400> 468
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 aggcacctc gccgtcctca 20

 <210> 470
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 <400> 470
 aaggccaagg tgagtccat 19

 <210> 471
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<213> Artificial Sequence

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 <400> 471
 cgagtgtgtg cgaaacctaa 20

 <210> 472
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 <212> DNA
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 <400> 472
 tcagggtcta catcagcctc ctgc 24

 <210> 473
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 <212> DNA
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 <400> 473
 aaggccaagg tgagtccat 19

 <210> 474
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 <400> 474
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 <210> 475
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 <213> Artificial Sequence

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 <400> 475
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 <210> 476
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 <212> DNA
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<220>

<223> Synthetic oligonucleotide probe

<400> 476

gggaggctta taggcccaat ctgg 24

<210> 477

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

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